

pgN1

1 GTCGAGGCAGTCACCTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT 69  
3 52 50  
Taql HindIII  
AluI

70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAAATTGATGGAGCTCTAAAGTTGCTGGCTGT 138  
89 95 119 121  
HhaI XbaI  
SacI  
AluI

139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATATAAATATTCTCTGAAAAGTGCTTTTGGCATA 207  
150 206  
NdeI

208 TGTAGGTTGGGCAAAACGAGGAAGATTGCTTCTCAATTGGAAGATGATGAACAGCCGAGAGAAAA 276

277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAAAGGTCGTCGTCCTCCCATGAACAGAGGT 345  
309 305  
Sau3AI  
DdeI

FIG. 1A

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EcRV

346 AACACATTTTGGCATATACACTTTGATAGTTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414  
408

415 CAATGTTGCAGAGACAANGCTGCGCJRRCATATACAGAAAGGGAATGAAGATGGCCCTTTTGATTAGCTG 483  
481  
469  
434 439  
440  
440  
441

AluI HhaI  
NaeI  
MspI  
HpaII  
HaeIII  
AluI

484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA 552  
498 535

AluI  
HinfI

553 TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATCTGATTGT 621  
564  
564 606

MspI  
HpaII  
HinfI

622 AGTAACTAAGAGAAGAACTTACCTTATGATTTCCTCCGAGGACTGGATTATGGAACAATGGGAAAGAAC 690  
629

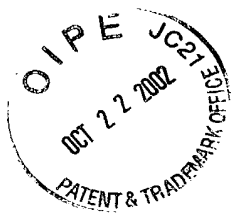
DdeI

FIG. 1B

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SacI  
691 TACTATATAAGCTCCATAGCGGGTTCAGATAACGGAGCTCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT 759  
AluI  
702 731  
760 TTAGTGAATAAATAACTTATTATCAAAAAGTCTTCATTGACTTATTATATATACTTGTGTGAATTGGTA 828  
AluI  
829 GGAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCATTCAAGTGGATAAAATAAGAAA 897  
DdeI  
843 866  
898 TGGAAAGAAGATTTTTCATGTAACTCCCATGACAACCTCGTGGTAATCGTTGGGGTGTGGTAATGTCGAGG 966  
XmnI  
909 962  
967 AACTCTGGCTTCTCTGATCAGGTAGGTTTTTTGTCTCTTATTGTCTGCTGTTTATTTTCCCTGATAG 1035  
Sau3AI  
982 982  
1036 TCTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTGTACCCCAAGCGATGGGATA 1104  
AluI  
1075 1088  
RsaI

FIG. 1C

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1105 CATAGGAGGTGGCAGAAATGGGTATAGATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTTCATA 1173  
Sau3AI AluI  
1156 1166

1174 TTAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCAACCGCCTTTCCAAAGT 1242  
HinfI  
1216

1243 ACTCATGTCAAGGTTGGTTTCCTTTAGCTTTGAACACACAGATTGGATCTTTTGTGTTTCCATATAC 1311  
ScaI AluI Sau3AI  
RsaI 1269 1286

1312 ATAGGACCTGAGAGCTTTTGGTTGAATTTTTTTTTTTTCAGGACAAATGGCGAAGAAATCTGTACATTG 1380  
DdeI AvaII AluI HinfI RsaI  
1316 1326 1368 1375

1381 CATCAATATGCTATGGCAGGACAGTGTGCTGATGATACACACTTAAGCATCATGTGTGTTAGAAAG 1449  
MstII DdeI Tth111I

1450 CCGAAGACAATTGGAGCGGAGCCCTCAGGGTGTGTCATAATACCAATCAAAGACGTAAACCAGACGAGTC 1518  
1472 1514

FIG. 1D

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1519 TCCTTGGTTGAATGTGATGAAAGGATGTGTCTTGGTATGATGTACGAGTAACAAAAGAGAGATGCA 1587  
1564  
RsaI

1588 ATTGAGTAGTAAAGATTTGAGAGCTTTTAAAGCCCTTCAAGTGTGTGCTTTTATCTTATTGATATC 1656  
1613 1619  
AluI DraI EcoRV

1657 ATCCATTGGCGTTGTTAAAGCGTCTTTAGATATGTTTCTGTTTCTTCTCAGTGTCTGAATATCTGAT 1725  
1706  
DdeI

1726 AAGTGCAATGTGAGAAAGCCACACCAACCAAAATATTCAAAATCTTATATTTTAAATAATGTCGAATCA 1794  
1790 1788  
TaqI  
HinfI

1795 CTCGGAGTTGCCACCTTCTGTGCCAATTGTGCTGAATCTATCACACTAAAAAACAATTTCTTCAAGGT 1863  
1829  
HinfI

1864 AATGACTTCTGGACTATGTTCTGAAATCTCAATTAAGTTTATTTTTTTGAAGTTTAAGTTTACCTTC 1932  
1887  
EcoRI

FIG. 1E

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1933 TTTTTTGAATAATATCGTTTCATAAGATGTCACGCCAGGACATGAGCTACACATCACATATTAGCATGCA 2001  
1968 1978 SphI  
BstNI AluI  
2002 GATCGGACGATTGTCACTCACTTCAAAACACCTAAAGAGCTTCTCTCTCACAGCACACACATATG 2070  
2043 NdeI  
AluI  
2071 CATGCAATATTTACACGTGATCGCCCATGCAAAATCTCCATTCTCACCTATAAATTAGAGGCTCGGCTTCA 2139  
2073 2075 SphI  
NsiI Sau3AI  
2140 CTTTTTACTCAAAACCAAACTCATCACTACAAACATACACAAATGGCGAACAAGCTCTTC 2200  
Met AluI  
2195

FIG. 1F

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Lambda CGNI-2  
NCG-186 Linear Length = 4325

XhoI  
TaqI  
AvaI  
||  
CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGGCCCAACTATGGGAAGCTTATTCTCTTTTCGAT 69  
2 3 50 52 66

HindIII  
AluI  
|  
TaqI  
|  
ACTCTAATTGAGCCGTCCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT 138  
89 95 119 121

HhaI XbaI  
|  
SacI  
AluI  
|  
TTTCTTGTTTCATATGATTAACTTCTAAACTTGTGTATAAAATATTCTCTGAAAGTGCTCTTTTGGCATA 207  
150 206

NdeI  
|  
TGTAGGTTGGGCAAAACGAGGAAGATTGCTTCTCAATTGGAAGAGGATGAACAGCCGGAAGAGAAA 276

Sau3AI  
DdeI  
|  
TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATATAACGGTCGTCGCCATGAACAGAGGT 345  
309 305

EcoRV  
|  
AAAACATTTTGGCATATACACTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414  
408

FIGURE 2A

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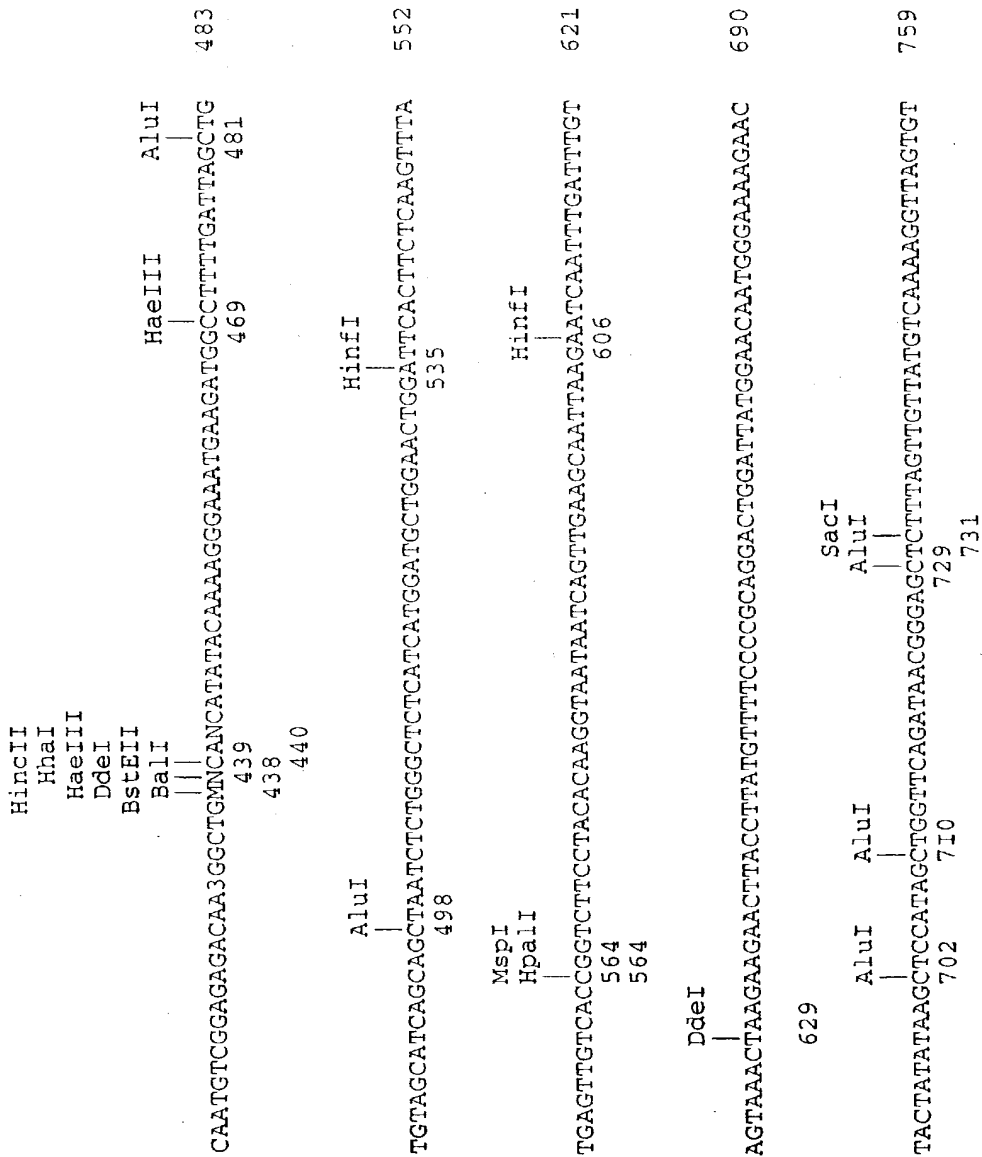


FIGURE 2B

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TTAGTGAATAAATACTTATACCAAGCTTTCATTGACTTATTTATATATACTTGTGTAATTGCTAG 828

DdeI HinfI

GAACTACTTATTTCTCAGCAGTCATACAAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT 897

842 865

XmnI TaqI

CGAAAGAAGATTTTTCATGTAAACCTCCATGACAACTGCTGGTAATCGTTGGGTGTGGTAATGTTCGAGGA 966

908 961

Sau3AI BclI

ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCGTGGTGTTTTATTTTCCCTGATAGT 1035

981

AluI RsaI

CTAATATGATAAACTCTCGGTTGTCAAAGGTGGTGGAGCTTTGACCTTTTGTACCCCAAGCGATGGGATAC 1104

1074 1087

Sau3AI AluI

ATAGGAGGTGGGAGAAATGGGTATAGAAATAACATCAATGGCAGCAACTGGCGGATCAAGCAGCTTTTCATAT 1173

1155 1165

HinfI ScaI RsaI

TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCCACCACCGCCTTTCCAAAGTA 1242

1215 1242

FIGURE 2C

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CTCATGTC AAGTTGGTTCTTTAGCTTTTGAACACAGATTGGATCTTTTGGTTTGTGTTTCCATATACT 1311  
 1268 1311  
 AluI Sau3AI DdeI  
 1285  
 TAGGACCTGAGAGCTTTTGGTTGATTTTTCAGGACAAATGGCGGAAGAATCTGTACATTGCATCA 1380  
 1315 1325 1363 1370  
 DdeI HinfI RsaI  
 1319  
 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAGCATCATGTGGAAGCCAAAGACAATTGGAG 1449  
 HinfI DdeI  
 CGAGACTCAGGTCGTCATAATAACCAATCAAGACGTTAAACCCAGACGCAACCTCTTTGGTTGAATGTA 1518  
 1456 1454  
 RsaI  
 ATGAAAGGGATGTGTCCTGGTATGTATGTACGAATAACAAAGAGAGATGGAATTAGTAGTAAATA 1587  
 1548  
 AluI EcoRV  
 TTTGGGAGCTTTTAAAGCCCTTCAAGTGTGCTTTTATCTTATTGATATCATCCATTGCGTTGTTAA 1656  
 1596 1635  
 XbaI DdeI  
 TCGCTCTCTAGATATGTTCCCTATATCTTTCTCAGTGTCTGTATAAGTGAATGTGAGAAAACCATACCAA 1725  
 1664 1687

FIGURE 2D

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Hinfi  
ACCAAAATATTCAAATCTTATTTTAAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATIG 1794  
1761  
HinfI  
TGCTGAATCTATCACACTAGAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC 1863  
1800  
EcoRI  
TCATTAAAGTTTATTTTCTGAAGTTTAAAGTTTACCTTCTGTGTTTGAATATATATCGTTTCATAAGATG 1932  
SphI  
BstNI AluI  
1940 1950  
SphI  
Sau3AI  
1971  
1973  
TACAGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTGTCACCTCACTTCAAA 2001  
DdeI AluI HhaI NdeI SphI  
2006 2012 2028 2036 2042 2044  
Sau3AI  
CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCCAATATTTACACGTCGCGCCATGCAA 2070  
2058  
AluI  
ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAAACCAAACTCATCTACA 2139  
2164  
DdeI AluI  
2006 2012 2028 2036 2042 2044  
Sau3AI  
GAACATACACAAATGGCGAACAAGCTTCTCTCGTCTCGGCAACTCTCGCCTTGTCTTCTTCTCACC 2208  
MetAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr

FIGURE 2E

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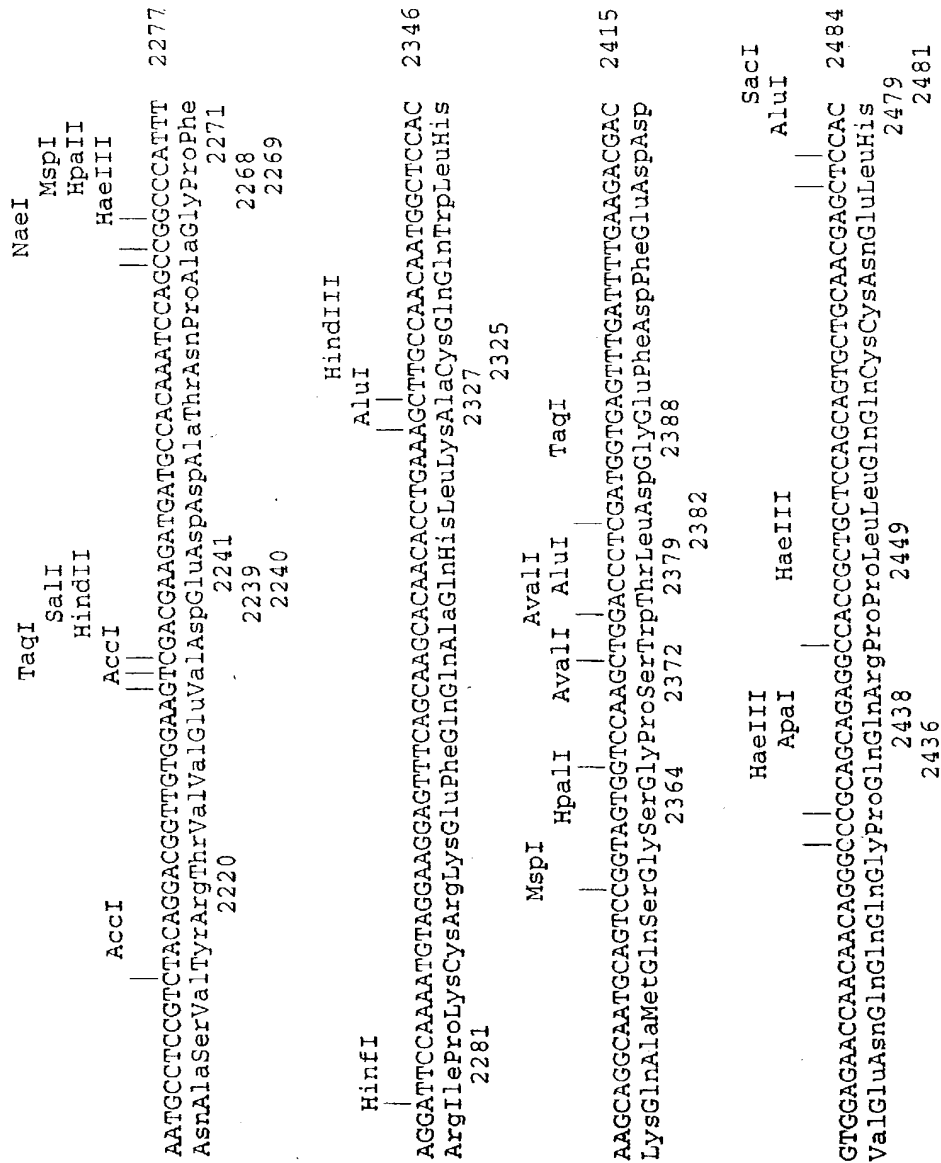


FIGURE 2F

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2553  
2548  
2486  
2551  
2622  
2639  
2688  
2760  
2736  
2724  
2725  
2707  
2694  
2692

BstNI  
HinfI  
TaqI  
AluI  
BstNI  
MspI  
HpaII  
HaeIII  
ApaI  
XhoI  
TaqI  
AvaI  
HinfI  
AccI  
ProGlyPheTyr  
ProGly

CAAGGAAGAGCCACTTTGGCGTTTGGCCCAACCTTGAAGGAGCATCCAAAGCCGTTAAACAACAGATTCTCGA  
GlnGluGluProLeuCysValCysProThrLeuLysGlyAlaSerLysAlaValLysGlnGlnIleArg  
CAACAACAGGGACAAACAATGCAGGGACAGCAGATGCAGCAAGTGATTAGCCGTATCTACCAGACCCGCT  
GlnGlnGlnGlyGlnMetGlnGlnMetGlnGlnMetGlnGlnValIleSerArgIleTyrGlnThrAla  
ACGCACTTACCTAGAGCTTGCAACATCAGGCAAGTTAGCATTTGCCCTTCCAGAGACCATGCCCTGGG  
ThrHisLeuProArgAlaCysAsnIleArgGlnValSerIleCysPropheGlnLysThrMetProGly  
CCCGGCTTCTACTAGATTCCAAACGAATATCCCTCGAGAGTGTTGTATACCAACGGTGATATGAGTGTGGTT  
ProGlyPheTyr

FIGURE 2G

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HindII		RsaI	
GTTGATGATATGTTAACACACTACATAGTCATGGTGTGTGTTCCATAAAATAATGTACTAATGTAATAAGAAC			2829
2771		2813	
AccI			
TACTCCGTAGACGGTAATAAAAAGAGAAAGTTTTTTTTTTTACTCTTGCTACTTTCCTATAAAAGTGATGAT			2898
2838			
		ScaI	
		RsaI	
TAACAACAGATACACCAAAAAGAAAAACAATTAACTATATTCCACAATGAAGCAGTACTAGTCTATTGAA			2967
		2954	
		Sau3AI	
CATGTCAGATTTTCTTTTCTAAATGTCTAATTAAGCCCTCAAGGCTAGTGTGATGATAAAAGATCATCCA			3036
		3028	
Sau3AI			
BamHI	HinfI		
ATGGGATCCCAACAAGACTCAAAATCTGGTTTTTGTATCAGATACTTCAAAAACATAATTTTGTATTCATTAAA			3105
3041	3053	3069	

**FIGURE 2H**

097042120 102500



09702130 102202

HinfI  
TTATGCAAGTGTCTCTTTATTTGGTGAAGACTCTTTAGAGCAAAACAACGACAAGCAGTAATAAAAAA 3174  
3135  
ACAAAAGTTCAGTTTAAAGATTGTTATTGACTTATTGCTATTGCAATTTGAAAAAATATAGTATGATATTATATA 3243  
GTTTTATTATATAATGCTTGTCTATTCAAGATTGAGAACATTAATATGATACGTGCCACATATCCAA 3312  
NdeI  
TATATTAAGTTTCATTTCTGTTCAAAACATATGATAAGATCGGTCAAAATGATTATGAGTTTGTATTAC 3381  
3341  
TaqI      Sau3AI  
AluI      RsaI  
CTGAAGAAAAGATAAGTGAGCTTTCGAGTTTCTGAGGGTACGTGATCTTTCATTCTTGGCTAAAAGCGA 3450  
3402      3421  
3405      3425  
ATATGACATCACCTAGAGAAAGCCGATAATAGTAAACTCTGTTCTTGGTTTTTGGTTTAAATCAAACCGA 3519  
MspI    DdeI  
HpaII   AluI      NdeI  
HinfI  
ACCGGTAGCTGAGTGTCAAGTCAGCAAAACATCCGAAACCATATGTCAATTCGTTAGATTCCCGGTTAA 3588  
3522    3528      3560      3576      3581  
3529

FIGURE 2I

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Mspl  
HpalI  
|  
GTTGTAAACCGGTATTTTCATTGTTGGTGAAACCCCTAGAACCCAGCCAGCCANCCCTTTTAAATCTAATTTTIGCA 3657  
3598

HinfI  
HincII  
|  
DdeI  
|  
BstNI  
|  
AACGAGAAGTCACCCACACCTCTCCACTAAACCCCTGAACCTTACTGAGAGAAGCCAGAGNCANNAAGAA 3726  
3702 3718  
3715  
3714

CAAAATAAAACCCGAAGATGAGACCAACACGTTGCGGGCGGACGTTTCAGGGGACGGGGAGGAAGAGAAATGR 3795

AvaII  
AluI  
|  
CGGCGG5MNTTGTGGTGGCGGCGGCGGACGTTTGTGGTGGCGGCGGTGGACGTTTGTGGTGGCGGCGGTGGA 3864  
3804 3863  
3801

EcoRV  
|  
AvaII  
|  
DdeI  
|  
CCTTTGGTGGTGGATATCGTGACGAAGGACCTCCACGTGAAGTCATTGGTTGCTTACTCTTTCTTAG 3933  
3880 3892 3930

FIGURE 2J

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TagI                      HindIII                      DdeI  
HinfI                      AluI  
|                      |                      |  
TCGAATCTTATTCTTGCTCTGCTCGTTGTTTACCGATAAAAGCTTAAGACTTTATTGATAAAGTTCTCA                      4002  
3937                      3976                      4000  
3935                      3974  
  
AluI                      XmnI                      HinfI                      DdeI  
|                      |                      |                      |  
GCTTTGAATGTGAATGAACGTGTTTCCCTGCTTATTAGTGTTCCCTTTGTTTGGAGTTGAATCACTGTCTTA                      4071  
4004                      4023                      4059                      4069  
  
HinfI  
|  
GCACTTTGTGTAGATTTCATCTTTTGTGTTTAAAGTTAAAGGTAGAAAACCTTTGTGACTTGTCTCCGTTATG                      4140  
4085  
  
HincII  
|  
ACAAGGTTAACTTTGTTGGTTATAACAGAAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG                      4209  
4146  
  
AvaI                      AluI                      DdeI                      Sau3AI  
|                      |                      |                      |  
GACCAAGCTCTCTCAGCGGAAGATCCCTTACTTCAATGCCCCAATCTACTTGGAAAACAAGACACAGAT                      4278  
4210                      4217                      4222                      4231

FIGURE 2K

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TaqI  
 SalI  
 PstI  
 HindIII  
 Sau3AI  
 AluI  
 HincII  
 AccI  
 EcoRI  
 TCGGAAAGTTGATGAGATCCAAAGCTTGGGCTGCAGGTCGACGAATTC  
 4294 4302 4316 4321  
 4300 4314 4313 4315

4325

FIGURE 2L

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*Brassica campestris* ACP Genomic Sequence

1 AAGAGTATGCTACTACTACTACTCTCTATAATCAAGTTTCAAGAAGCTGAGCTTGGCTCTCACTTTATAT 69  
11 46 51  
47  
70 GTTTGATGTTGTTGTCAGGATGGTAAATCATGGAAGAGATAAAGAATGCAAAACCTGAAGTATTGG 138  
139 CAGAGAGGACTGAGGTGAGAGAGCATGTCACCTTTTGTGTTACTCATCTGAATTATCTTATATGCCAATT 207  
149  
208 GTAAAGTGGTACTAAAGGTTTGTAACTTTTGGTAGGTGGATTTGAAGGATAAATGGAGGAACCTTGCTTC 276  
217  
277 GGTAGCGGTAACAAGTTTTATATTGCTATGAAGCTTTTTCCTGCGTGACGTATCAGCAGCTGTGGAG 345  
310  
338  
338

AccI  
DdeI  
AluI AluI  
HindIII  
AluI  
PvuII

FIGURE 3A

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346 AAGATGGTATTAGAAAGGGTCTTTTTCACATTTTGTGTGTGTGACAAATATAATTCCGCCCGGTATGGTTT 414  
MspI  
HpaII  
HaeIII  
403  
404  
404

415 GGTTAAGACTTGTTGAGAGACGCTGTGGGGTTTTTTTGTATGTATAATTAGTCGTGTGTAGAACGAAACAA 483

484 GACTTGTGNGTATGCTTTTTTTTAACTGACGGGGTTTTGTGTGTGTAGTTAGGAACCTTGACTTTGTCT 552  
Tth1111I  
547

553 CTTTCTCTCAAGATCTGATTGGTAAGGCTCTGGGTGGTAGTACTGTTTGGTTTAAATTTTGTGACTATT 621  
ScaI  
RsaI  
564  
564  
593  
593

622 GAGTCACTGTGGCCCCATTGACTTTTAAATTAGGCTGGTATATTTTTTTTGGTTTAAACCGGTCTCAGATAG 690  
HinfI  
HaeIII  
DraI  
HpaII  
DraI  
MspI  
DdeI  
623  
634  
646  
673  
678  
683  
678

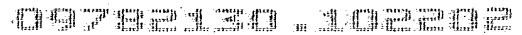
FIGURE 3B

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**FIGURE 3C**

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HaeIII HindIII  
| |  
967 AAGGCCCATGTTATCATAAAACGCCGTCGTTTTGAGTGCACCAAGCTTATAAATGTAGCCAGCTACCTC 1035  
971 1012 1029 1034  
1010  
AluI AvaI  
| |  
1036 GGGACATCAGCGCTCTTTGTACACTCCGCCCATCTCTCTCTCTCGAGCAGATCTCTCTCGGGAATATCG 1104  
1055 1078 1085 1093 1103  
1079 1085  
1078  
RsaI XhoI  
| | |  
1105 ACAATGTCGACCACTTTCTGCTCTTCCGTCCTCCATGCAAGCCACTTCTCTGGTAATCTCATCTCCTTCT 1173  
1112  
1110  
1111  
1112  
1108  
Tth1111  
TaqI  
Sali  
HincII  
AccI  
| | |  
METSerThrThrPheCysSerSerValSerMETGlnAlaThrSerLeu

FIGURE 3D

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1174 TGTGTTCCAGATCGCTCTGATCATACCTTCTTTTAGATCATTTGGCCTCTGATCTGTGCTTGATGTTT 1242  
Sau3AI BclI Sau3AI  
1184 1193 1210 1224  
1193  
HincII AluI HinfI  
1243 GTTAACCTCTCCACGCATGTTTGATTATGTTGAGAAATTAGAAAAAATGTTAGCTTTACGAAATCTTTAG 1311  
1243 1296 1303  
Sau3AI BclI TaqI Sau3AI  
1312 TGATCATTTCAATTGGATTGCAATCTTGTGTGACATTTGAGGCTTGTGTAGATTTCCGATCTGTATTCA 1380  
1313 1369 1368  
1313  
HinfI AluI DraI  
1381 TTTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGTGTTTTTAAATGAACATGTTTGTGTATTGA 1449  
1386 1394 1425  
AluI  
1450 TGGACAAACAGGCAGCAACAACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTC 1518  
AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu  
1496

FIGURE 3E

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1519 TCCTTCAACCTCCGCCGTTCAATCCCACTCGTTTCTCAATCTCCTGCGCGGTATGTTCTCATTTCTCAG 1587  
SerPheAsnLeuArgSerIleProThrArgPheSerIleSerCysAla 1568  
HhaI DdeI  
1584  
TaqI  
1597  
1601  
1616  
1648  
1656  
1676  
1695  
1725  
1743  
1756  
1763  
1837  
1852  
1863

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FIGURE 3F





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1864 GTGATGGGTTTAGAGGAAGAGTTTGATATCGAAATGGCTCAAGAGAAAGCTCAGAGATTGCTACTGTG 1932  
ValMetGlyLeuGluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrVal  
1891 1893 1914 1914  
1893  
1933 GAGGAAGCTGCTGAACCTCATTGAAGAGCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAAGAGCAGCCA 2001  
GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLysLys  
1940 1960 1962  
2002 AGGCTTTGTTGGTTTGTTGTTTTCATAATCTTCCTGTCATTTTCTTTTCTTTAAATGTGTCAAGCGAC 2070  
2069  
2071 TCTGTTGGTTTAAAGTAGTATCTGTTTGGCCATGGATCTCTCTCTCTATTGTCGACTGAAAACTTTTGGTT 2139  
2082 2100 2104 2119 2120 2121  
2140 TACACATGAAAGCTT 2154  
2152 2150  
2150

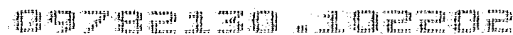
DdeI  
AluI  
TaqI  
EcoRV  
SacI  
AluI  
AluI  
DraI  
HindIII  
AluI  
Sau3AI  
NcoI  
TaqI  
SalI  
HincII  
AccI

FIGURE 3G

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Complete nucleotide sequence of B. campestris cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

**FIGURE 4A**

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208	ACGCAACGTGGAACCGCATTGAACGCTTAATGACGTTCAATCCGGACTAACGTTTAAACTCGGGTGAA	276	
	sArgAsnValGluArgIleGluArgLeuAsnAspValGlnSerGlyLeuThrPheLysLeuAlaValAs	263	
		250	HpaII
			DraI
277	CCAGTTTGCTGATCTAACCAACGAAGAATCCGTTCTATGTACACTGGTTTCAAGGAACTCTGTGTT	345	
	nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyrThrGlyPheLysGlyAsnSerValle	318	
		303	EcoRI
		287	Sau3AI
			RsaI
346	GTCTAGTCGAACCTAACCAACGTCGTTTAGGTACCAAAACGTTTCTTCTGATGCGTTGCCGGTTTCTGT	414	
	uSerSerArgThrLysProThrSerPheArgTyrGlnAsnValSerSerAspAlaLeuProValSerVa	405	
		380	RsaI
		378	KpnI
			HpaII
415	TGATTGGAGGAAGAAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTGGCGGTT	483	
	lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh	468	
		452	Sau3AI
		435	AluI

FIGURE 4B

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484 TTCAGCTGTTGGGCTATAGAGGAGTAGCACAGATAAAGAAAGGAAACTCATTTCTTTGTCTGAACA 552  
eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysGlyLysLeuIleSerLeuSerGluGly  
489  
489

553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGCGGTTTGTGATGATACAGCGTTTAACTA 621  
nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy  
557 562  
560  
561  
562

622 CACAAATAACTATTGGCGGCTTAACCTCTGAATCAATTAATTCCTTATAAAGCACAAACGGCATTGCAA 690  
rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyProTyLysSerThrAsnGlyThrCysAs  
HpaII  
691 CTTCAATAAAACTAAACAGATAGCAACTTCTATCAAAAGGTTTGTAGGATGTCCCGGCTAACGATGAGAA 759  
nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy  
744

FIGURE 4C

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760 AGCCCTAATGAAGCAGTGGCACACACCCGGTTAGCATTTGGAATAGCGGAGGAGATATTGGTTTCCA 828  
sAlaLeuMETLysAlaValAlaHisHisProValSerIleGlyIleAlaGlyGlyAspIleGlyPheG1  
789 HpaII

829 ATTCTATTCTCGTCCGGTGTGTTTCAGCGGAGAATGCACAATCATCTTGTATCAGGGGTAACGTGGTTGG 897  
nPhETyrSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValG1  
841 875 875  
HpaII Sau3AI  
BclI

898 ATACGGCCGATCTAAAACGGATTAAAGTACTGGATCCTCAAGAAATTCATCGGGACCAAAATGGGGAGA 966  
yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyG1  
904 931 941 951  
ScaI Sau3AI  
RsaI EcoRI AvaII  
HaeIII BamHI

967 ACGTGGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGCAATGC 1035  
uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl  
982 995  
Sau3AI EcoRV

FIGURE 4D

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Rsal | HindIII  
 HpaII | AluI  
 1036 TTCGTACCCCACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAAATAAAATGCTGTGTTGG 1104  
 aSerTyrProThrMET  
 1041 1073 1081  
 1079

1105 TTATAATTTAAGACTCTGTGTTGCCATGTAATTTGTGAAATGGTAAGTTTATGTGATGCCAAAAGATTTGATA 1173

1174 AAAAAAAAAAAAAA 1186

FIGURE 4E

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3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51  
3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102  
3H11 CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153  
3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204  
TGCTCATCAATTAGCAATTAATCC  
3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255  
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC  
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe  
3H11 GTTGTTCCTTTTGACGACCACCTTTAGTTGATATGTCTGGAATTTGAAAAATG 306  
2A11 GTTGTTCCTTTTGACGACCACCTTTAGTTGATATGTCTGGAATTTGAAAAATG  
ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET  
3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAAATG 357  
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAAATG  
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET  
3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408  
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA  
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer  
3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459  
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG  
AsnSerAspCysIleGlyIleThrLeuCysGlnPhyCysLysGluLysThr  
3H11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCCTTGAACAATA 510  
2A11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCCTTGAACAATA  
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro  
3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561  
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA  
3H11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612  
2A11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATGTGAATAAAGGGATACATAT  
3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663  
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT  
3H11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATCCACATTAAT 714  
2A11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTC  
3H11 TCACGTATTTATTTCACTTATGATACGTATTTTTGTTCCTTTGCGGTAAAA 765  
3H11 AAAAAAAAAA 774

FIGURE 5

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(a)

2A11

PA1b

Chick pea  
inhibitorLima bean  
inhibitor $\alpha_1$ -antitrypsin

V	M	A	L	R	D	I	P	P	Q	E	T	L	L				
V	C	S	P	F	D	I	P	P	C	G	S	P	L	C	R	C	I
V	C	T	-	K	S	I	P	P	-	-	-	-	Q	C	R	C	N
L	C	T	-	K	S	I	P	P	-	-	-	-	Q	C	R	C	T
L	G	A	I	P	M	S	I	P	P	E	V						

(b)

2A11

PA1b

Barley chloroform/  
methanol-soluble  
protein dWheat  $\alpha$ -amylase  
inhibitor 0.28

Wheat albumin

Millet bi-functional  
inhibitorCastor bean 2S  
small subunit

Napin small subunit

T	N	I	L	G	L	C	N	E	P	C	S	S	N	S	D	C	I	
G	S	P	L	C	R	C	I	P	A	G	L	V	I	G	N	C	R	
T	N	L	L	G	N	C	R	-	F	Y	L	V	Q	Q	T	C	A	
V	S	A	L	T	G	C	R	-	A	M	V	K	L	Q	-	C	V	
V	P	A	L	P	A	C	R	P	L	-	L	R	L	Q	-	C	N	
N	N	P	L	D	S	C	R	W	Y	V	S	A	T	K	R	A	C	G
Q	Q	N	L	R	Q	C	Q	E	Y	I	K	Q	Q	V	S	G	Q	
A	Q	N	L	R	A	C	Q	Q	W	L	N	K	Q	A	M	Q	S	

FIGURE 6

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2A11 GENOMIC

CTCGAGCCCT TTAAAAAGTA TAGTCAATAT TTACGGTGAC CGTGAATTC TTAAATTATGA 60  
TATATAATTT AAAAGAAATC ATGATCACAT TCTACTGATG AGAACATGTG CTAAATCAAGG 120  
GAAAACATGG ATGTGAAAAA TACTTTTTGT TAAAAAGTAAA AAAAAATGTG AAATTTTGT 180  
AGTTATTAC TACCTATACA TTATTTGAGC ATGTGCAAAC TTTACAAAATA CCTAATAGAA 240  
GATTTTCACC TGCCTGTATA TATGTAAAT TATTATAATG AACACTCTCA CATAAAAATA 300  
TTATCAGTAT ATACATTAACT ACTTGCCCTC CACAATGAAT TAAATAAAT GTAGAACATG 360  
ATCTACACTT CAATAAAACT AAGACCATAA AGAATAATTT CAAAATATAC ACATGTCAAC 420  
AATAAATTAT TTGCATATTA TATTAACTTA CTAAACAATC TTTACTTTTG AAATATAAAA 480  
ATAATCAAGT TATAAGTCTG CTCAAAAGTAA AGCACTTGTT AGACTCATCT GATTTTGAGA 540  
AGGTAAGCAA ATTGATGGTG CATAATAGTC ACAAGTAAAA TATAAATAG ATTTCATTAG 600  
TAAAAATTGTT TTTTACTTTC TTTATATATA ATTATCAATA TCCTTCAATG GTAGGTTAAT 660  
TATATTTGTTA ACTTCTTGTT GAATTAAAGC AATAAGACAA GAATATTAAA GATAAAAGAA 720  
CAATAAAAAAT AGAAAGACTA AGAGATAAGA GTTTTCTTAT TCTTCTTTCA ATAAGTATCA 780  
TCAGTGTAT ACAATATAAA TTTTGTGATT TTGATCTAT CTATTTATAA TGTATATAT 840  
AAGCATACAA AAGATCAGTC ATAAATATGA CTTTAATCAT GAAAATAATG AAAGAGATTA 900

FIGURE 7A

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05782130 . 102202

960 TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAATAAAA GGGGTTATCT TTATAATTGA  
1020 ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT TTTTTTAAAA AAATGGACAT  
1080 TTACACTATA ATATTTTATA ACACTTTCCC TTAAACATCT AGGTATAAAT AATGAGTCTT  
1140 GTCAAAATCT TAGTAGGAAA AATTCTGTGA AATTTTTTTA GTGAAAACAA ATGATATATA  
1200 TATCTTGAAT ACTCATTATT TGTGTCTCA TTAAAAATCT TATCTGACCT ATAAAAATAA  
1260 TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAAATTA GTATAATTAT TAGTGAATAT  
1320 TTAATTAACA TAATTGTATA CTAAGGGCCC TATAAATTGG ATTCTTCTCA AAGAAAAATA  
1378 AAATCACCAC ACAACTTTCT TCTTCTGCTC ATCAATTAGC AATTAATCCA AAACCATT  
1426 ATG GCT GCC AAA AAT TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT  
MET Ala Ala Lys Asn Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val  
1474 CTT TTG ACG ACC ACT TTA GGTTCAACAAC ACTTCTCCCT TATTTTGTTT  
Leu Leu Thr Thr Thr Leu  
1534 TCTTAATTTC TTGGAAGTCA TATGCATGTG TTTGGTATCA TGGTATATAT ATAAAGGAAA  
1594 ATATTTTCTT TAATTACTGG TTTTCTAATG TTTGGTAGGT AATCGGAAAT TATTATGAGA  
1654 TAATGAACTT GCAAAGTCAT TATTATATAA CTTTTTTTTT ATACTTTGAT TTAAGAAATTC  
1714 ATTTTCTCTA TTTTATATAA ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA  
1774 CACACCCCTAA GACATTACAT ATATATATAT ATACACCCCTC CGTTTATAT TACTTAATGC

FIGURE 7B

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09702130 . HORDON

CTATTGAGTT GGGCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT ACTAAATTAA 1834  
CCTATGCTTT AAGACTCTAA ATTGGCTAT TACTATTTTA CGTTGTAATT TAATGACAAA 1894  
CATTTCATAA TGACTATAGT CTGAACCTAA TTAGACAGAC GTATCTATAG TTTGCTTACT 1954  
AATGATTCAAT AGCTATATAT TTGGAGAGGA GAGAGACAAA CGATATTAAAG AAAGGGAGGA 2014  
GAGAGGGCAG GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA 2074  
TACTTTTGAT TATTATTTTT ATTATATGTA CGTTTACATT ACAGTTTTCG AATTCTTACA 2134  
TTAATCTTAA TCATAATATA TACA GTT GAT ATG TCT GGA ATT TCG AAA ATG CAA 2188  
Val Asp MET Ser Gly Ile Ser Lys MET Gln  
GTG ATG GCT CTT CGA GAC ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG 2236  
Val MET Ala Leu Arg Asp Ile Pro pro Gln Glu Thr Leu Lys MET  
AAG CTA CTT CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC 2284  
Lys Leu Leu Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser  
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT TGT AAG GAG 2332  
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe Cys Lys Glu  
AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT ACA TGC AAC CTG TTG CCT 2390  
Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg Thr Cys Asn Leu Leu Pro  
TGA ACAATATCAA TGATCTATCG ATCGATCTAT CTATCTATTT ATCTGTCTCT 2433  
GGCGGTATAG TGTGTCTCTGT ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT 2493  
CTAGATATAT TCTAGGTAAT GTCCTATTGT ATTAAAAATT TGTAGCAATG ATTGTTTGAA 2553

FIGURE 7C

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TAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAT TCACGTATTT ATTTCACTTA 2613  
TGATACGTAT TTTTGTTCCT TTGCGGTAGA TTTTGTGATCC TTTTCCCTTT TGAATATTAA 2673  
ACATTAAACA CAAATAATGT TTATTAAATT AAGTTAATAT TTTTATTTAG CTATTTTATAT 2733  
TTTTATTTGA AATCAAACTT GATAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC 2793  
TAACACCATG TAATATTATC TTGTCGTTAT TTATGATAAT ATTTTAAAAAT TATAATTTCA 2853  
GTTAAAAAAT TATTAAAAAA ACATACTTTT AAAAAAGTGAG TTAGCCTCCG CTACCCACAT 2913  
ACTTATGAAT TGGACTAGTT GTTTTTTTGAC CCACAAAAAG AATGGGCTAA TTAAACCTGA 2973  
CCTATCAAAT TTCAGAAATCT GCATAGATTA GTCCGAACGA AATGAGTCAG CCCGTATTGA 3033  
ACAAAAATATC AACAAAGGAG TTATGTAAAG ATGTTTAAAG AGGAAAAAAG ATTTCTAATA 3093  
CATATGGACT TTCAATATCC CAACTTTGTG TGGCGATCTG AACCTGCTT AGTTTGTGA 3153  
TCATTAACTT GTCTTGCTAT GTATTTAAAG TTAAACITTT ATATGTTTAA ACTTACAGAA 3213  
AATACATATA AATCTCTCAA GACTTGGCAA CATAATTAC TTAGTACTT AAACACATG 3273  
AAAAATTTAA TATCCTTTTA ACATCTTTGA AGTGAATTAA ATTATCACA TCCGAGCCTA 3333  
CACCTTGGAC GTGGCCGGCA CTCAGAACC AGTGCCTGTC CCCAAGCTAA CCTCATCCT 3393  
GACTGACTAC AAGCGGAAGG CTAACCTAAG TATACAAAAAG CTTAAAACTG AATAAAATA 3453  
ACTTTACAAG GTTTTAAACAC AAATGAACAA CTTTGAAGAA AATAATATAT TCAACTAGCC 3513

FIGURE 7D

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ATAAAATAGA CAACTTTAGT CTTTAAAACA TTTAATAAAA TAAATGCAAA ATATAGACTC 3573  
CTTAACATAA CTGACTATCT ATGGAGCCTC TAATTGATAA AGATGGAAGT CCGGACAAGA 3633  
CCACGACATC CTGACTAAAC TGAGAAAGTAA ATAAAATCCC CCGGAAAAAA AGGAGCCTCA 3693  
CCATGGCTAA CTCGAACTCG GGGATATATC AATGAAGCTC CTGTTGATGA TCTTGAAGAC 3753  
ATGTCCTCTGC ATCATCAAAA AGATGCAGGC CAAATGGCTC AGTACGTAAA ATGTACGAGT 3813  
ATGTAAGGGA AATTCTAAAG TATAACATAA GCTTGATACT TGAATAAAAAG GAAACATACT 3873  
TACCTCTTTT CAACTCAACT CAAATTAAGA ATAAGATACT CAACTCAAAG ATTAGGTATT 3933  
CAACGCAAAT ATGGCACTCT ACTCAATGAA GTACAAATTA ACTCAGGATA CTCGACTTAA 3993  
GATACTCAAC TCCCGACACT CAACTGAACT CATTCAATA TAAAGCAGCT TAAAAACAAGT 4053  
TCAGTATAAA GTAAAGTTGT TTAAAAACAT GATGTCAACT CTGTGTGTAT AATAAGGGAT 4113  
ACAACATAAC TTTGAAATGT ATATAAAAAT ACAATTAACT GATGTATATA AAAATACATT 4173  
AATCTATGGG AGATTCTCTA ACCGACAACC ATCACTTAAG GGCTAAGATG ATGATATAGC 4233  
GATCTACCGC ACGCTGCCAT CGCATCTTAT ACCCGGCCAA AGGTATAAGA CCTGAACCTGC 4293  
CTAATGAATC CACTAATAAA CTGTTAAAAAG GAATCATCTA AAAAGTATGA CCCTTTTCTA 4353  
CCCATAGTGG CTAACATGGT TTATGGGGGC TGTGAGTTAT CTGAACCTCTC CCCCATATCG 4413

FIGURE 7E

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GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT	TAAAAACATA	CTGATTCTGT	4473
GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT	TTTGAAAAGC	TCTCTTTTGA	AAATCGTAGT	4533
TTCCCTTTTTC	TTCTATTAAA	GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTTCCTT	4593
CTCAAAAGTT	TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTTGGAA	4653
TTC						4656

FIGURE 7F

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## PG GENOMIC

10	20	30	40	50	60
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT ATAACAGTGG					
70	80	90	100	110	120
TAAAGCACCT TAAGAAACCA TAGTTTGAAA GGTTACCAAT GCGCTATATA TTAATCAACT					
130	140	150	160	170	180
TGATAATATA AAAAAAATTT CAATTCGAAA AGGGCCTAAA ATATTCTCAA AGTATTCGAA					
190	200	210	220	230	240
ATGGTACAAA ACTACCATCC GTCCACCTAT TGACTCCAAA ATAAAAATTAT TATCCACCTT					
250	260	270	280	290	300
TGAGTTTAAA ATTGACTACT TATATAACAA TTCTAAATTT AACTATTTT AATACTTTTA					
310	320	330	340	350	360
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTTA TGAATATCAT TTATAAACCA					
370	380	390	400	410	420
ACCAACTACC AACTCATTAA TCATTAAATC CCACCCAAAT TCTACTATCA AAATTGTCCCT					
430	440	450	460	470	480
AAACACTACT AAAACAAGAC GAAATTGTTC GAGTCCGAAT CGAAGCACCA ATCTAATTTA					
490	500	510	520	530	540
GGTTGAGCCG CATATTTAGG AGGACACTTT CAATAGTATT TTTTTC AAGC ATGAATTTGA					
550	560	570	580	590	600
AATTTAAGAT TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCATGCC TTTTTTAAAT					
610	620	630	640	650	660
ATAATTATAT AAATATTTAT GATTTGTTTT AAATATTAAA ACTTGAATAT ATTATTTTTT					
670	680	690	700	710	720
TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA AGGAATAATT AAGATGAACA					
730	740	750	760	770	780
TAGTGTTTAA TTAGTAATGG ATGGGTAGTA AATTTATTTA TAAATTATAT CAATAAGTTA					
790	800	810	820	830	840
AATTATAACA AATATTTGAG CGCCATGTAT TTTAAAAAAT ATTAAATAGT TTGAATTTAA					

FIGURE 8A

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850	860	870	880	890	900
					*
AACCGTTAGA TAAATGGTCA ATTTTGAACC CAAAAGTGGG TGAGAAGGGT ATTTTAGAGC					
910	920	930	940	950	960
					*
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG GATAATTTTG					
970	980	990	1000	1010	1020
					*
TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC CCTTCTTTAG TTTATAGACT					
1030	1040	1050	1060	1070	1080
					*
ATAGTGTTAG TTCATCGAAT ATCATCTATT ATTTCCGTCT TAAATTATTT TTTATTTTAT					
1090	1100	1110	1120	1130	1140
					*
AAATTTTSTA AAAATAAATT ATTTTSTCCA TTAACTTTTG ATTGTAATTA ATTTTSTAAA					
1150	1160	1170	1180	1190	1200
					*
ATTACCAACA TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTSTTA					
1210	1220	1230	1240	1250	1260
					*
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA AAAATTGAGA					
1270	1280	1290	1300	1310	1320
					*
CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAACTCT TTCGTCTAAA TATCTCTCAT					
1330	1340	1350	1360	1370	1380
					*
CCAAACTAAT ATAATACCCA TTATAATTAA CCATATTGAC CAACTCAAAC CCCTTAAAT					
1390	1400	1410	1420	1430	1440
					*
CTATAAATAG ACAAACCCTT CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTCA					
1450	1460	1470	1480	1490	1500
					*
ATAGACAAGT TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT					
1510	1520	1530	1540	1550	1560
					*
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCOA CTTGTAGAAG CAATGTTATT					
1570	1580	1590	1600	1610	1620
					*
GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG AACAAGAATT TGCTCATGAT					
1630	1640	1650	1660	1670	1680
					*
TTTCAAGCTT ATCTTTCTTA TTTGAGCAA AATATTGAAA GCAACAATAA TATTGACAAG					

FIGURE 8B

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1690	1700	1710	1720	1730	1740
					*
GTTGATAAAA ATGGGATTAA AGTGATTAAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA					
1750	1760	1770	1780	1790	1800
					*
AAAACATATG ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAAT					
1810	1820	1830	1840	1850	1860
					*
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA AGTAGAAAAT					
1870	1880	1890	1900	1910	1920
					*
TATTTTCTCG TTTTATAGTA TTAAAGGTGA AAAATGAGTT TTCTCGTAAG CGAGGAAAGT					
1930	1940	1950	1960	1970	1980
					*
CATTTTCCAT GGAACGTAT TTTTTTTTTTA CTTTAAATAA CGTCATAGTA TTTGCTATAC					
1990	2000	2010	2020	2030	2040
					*
TCAAGAATAA GACACTATTA TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG					
2050	2060	2070	2080	2090	2100
					*
CTAATATAAC TATCAATTTC TTATATGTAT ATTTTCAAC CAAAATAACA AAGCGTAATC					
2110	2120	2130	2140	2150	2160
					*
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT TATTTAATTT					
2170	2180	2190	2200		
TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT CGAATTC					

FIGURE 8C

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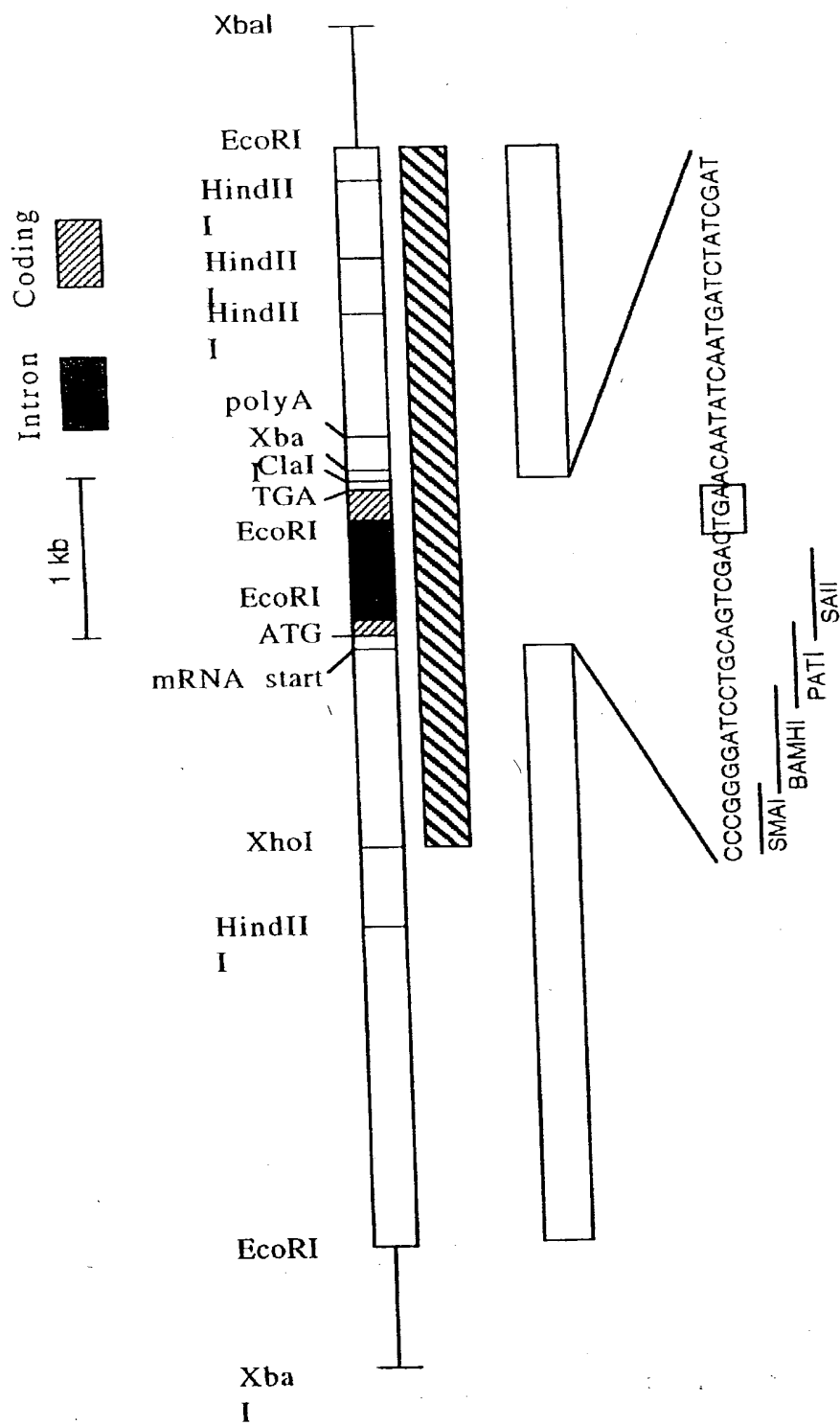


FIGURE 9

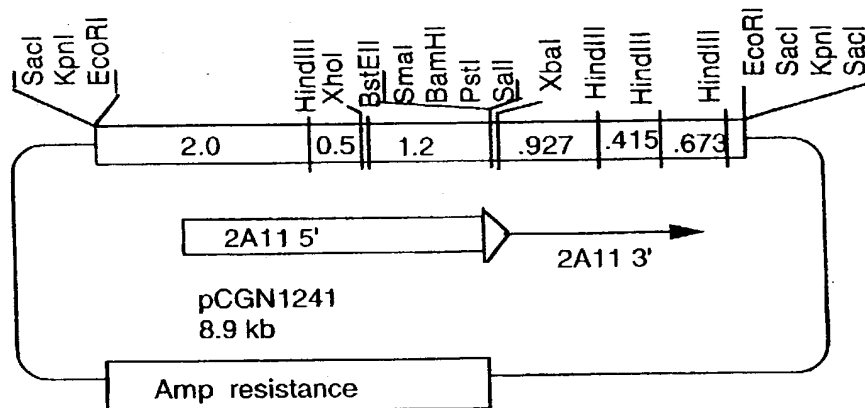
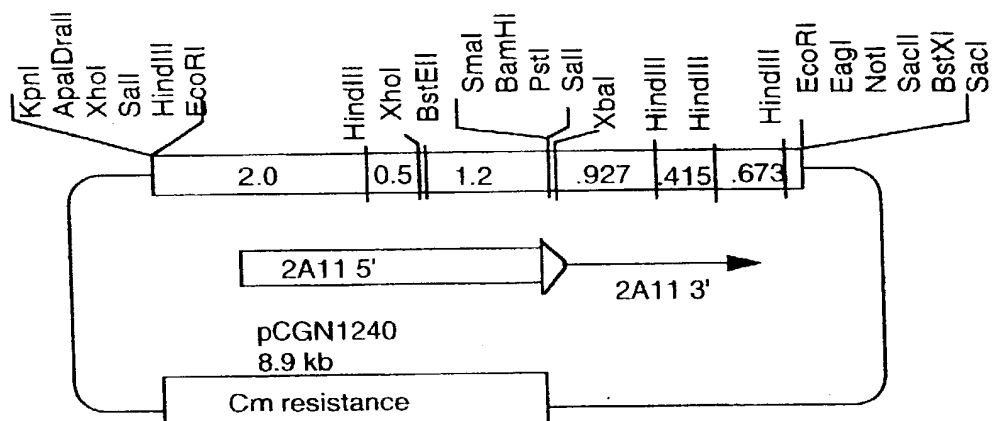
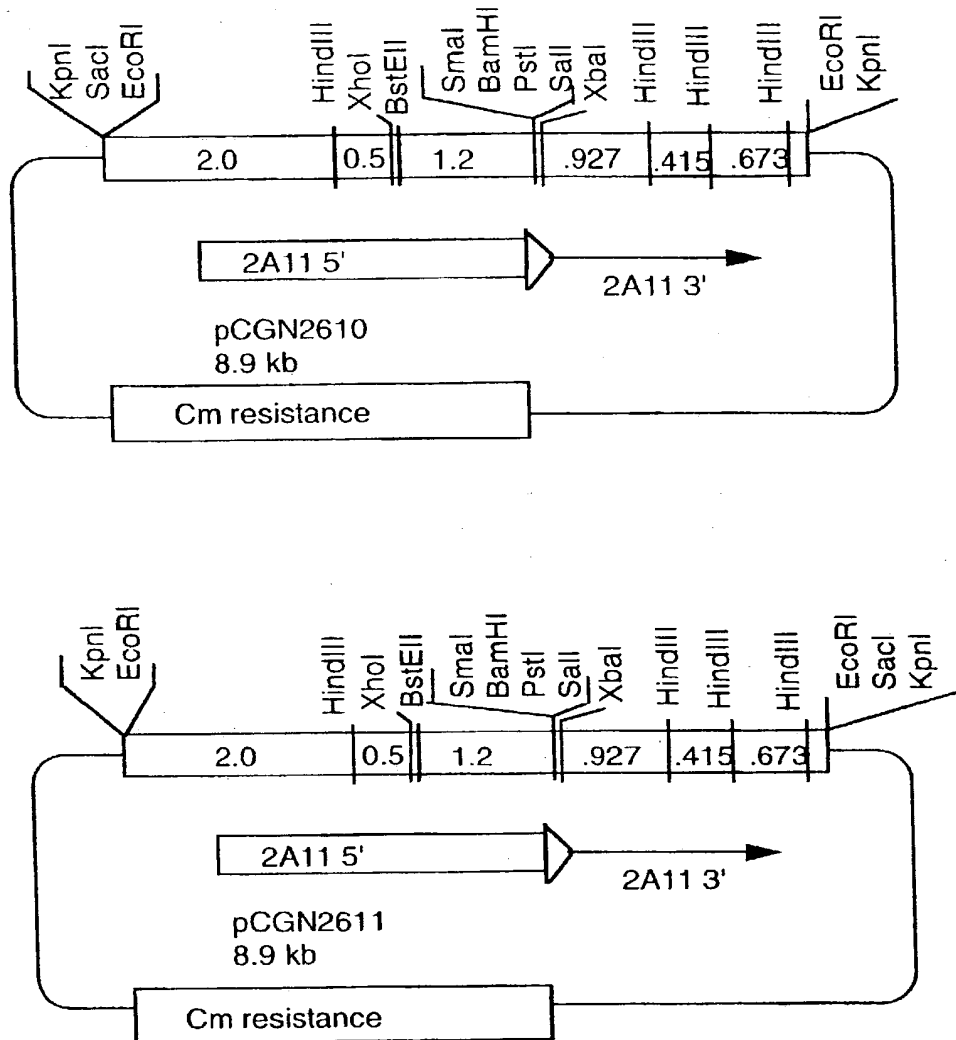


FIGURE 10A

**FIGURE 10B**